

SEQUENCE LISTING

<110> Heintz, Nicholas
Houchens, Christopher

<120> RIP60 Nucleic Acid and Polypeptide Sequences and Uses Therefor

<130> V0139/7038 (HCL/MAT)

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<151> 1999-01-04

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gaagaaccatgcctgaa cgtcgttgcaggggcccccctggccatgtggcctgtg 171
Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Leu

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Gln Ser Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys
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 Arg Arg His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg
 65 70 75

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 Cys Gln Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe
 80 85 90

cgc cat gcc ccc ttc tta gca ctg cac cgc cag gtc cat gct gct gcc 459

Arg His Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala	95	100	105	110	
acc cca gac ctg ggc ttt gcc tgc cac ctc tgt ggg cag agc ttc cga					507
Thr Pro Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg	115		120	125	
ggc tgg gtg gcc ctg gtt ctg cat ctg ctg gcc cat tca gct gca aag					555
Gly Trp Val Ala Leu Val Leu His Leu Ala His Ser Ala Ala Lys	130	135	140		
caa ccc atc gct tgt ccc aaa tgc gag aga cgc ttc tgg cga cga aag					603
Gln Pro Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys	145	150	155		
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Gln Leu Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala	160	165	170		
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Arg Pro Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp	175	180	185	190	
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Gln Leu Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu	195	200	205		
gcc gca gcc aag gct ctg ggg ccc cgg ccc agg ggc cgc ccc gcg gtg					795
Ala Ala Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val	210	215	220		
acc gcc ccc cgg ccc ggt gga gat gcc gtc gac cgc ccc ttc cag tgt					843
Thr Ala Pro Arg Pro Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys	225	230	235		
gcc tgt tgt ggc aag cgc ttc cgg cac aag ccc aac ttg atc gct cac					891
Ala Cys Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His	240	245	250		
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Arg Arg Val His Thr Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly	255	260	265	270	
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Lys Arg Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His	275	280	285		
acc ggc gag aag ccc tac ccc tgc aaa gag tgc ggc cgc cgc ttc cgg					1035
Thr Gly Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg	290	295	300		
cac aaa ccc aac ctg ctg tct cac agc aag att cac aag cga tcc gag					1083
His Lys Pro Asn Leu Leu Ser His Ser Lys Ile His Lys Arg Ser Glu	305	310	315		
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Gly Ser Ala Gln Ala Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala	320	325	330		

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cgc atc cac acc ggc gag aag ccc tac gtc tgc ccc gac tgc ggc aaa Arg Ile His Thr Gly Glu Lys Pro Tyr Val Cys Pro Asp Cys Gly Lys 480 485 490	1611
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35 40 45
Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys Arg Arg
50 55 60
His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg Cys Gln
65 70 75 80
Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe Arg His
85 90 95
Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala Thr Pro
100 105 110
Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg Gly Trp
115 120 125
Val Ala Leu Val Leu His Leu Leu Ala His Ser Ala Ala Lys Gln Pro
130 135 140
Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys Gln Leu
145 150 155 160
Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala Arg Pro
165 170 175
Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp Gln Leu
180 185 190
Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Ala Ala
195 200 205
Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val Thr Ala
210 215 220
Pro Arg Pro Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys Ala Cys
225 230 235 240
Cys Gly Lys Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg
245 250 255

Val His Thr Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly Lys Arg
260 265 270
Phe Thr Asn Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly
275 280 285
Glu Lys Pro Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys
290 295 300
Pro Asn Leu Leu Ser His Ser Lys Ile His Lys Arg Ser Glu Gly Ser
305 310 315 320
Ala Gln Ala Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala Gly Pro
325 330 335
Gln Glu Ser Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys Pro Ala
340 345 350
Gln Glu Pro Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp Pro Ile
355 360 365
Glu Ala Pro Pro Ser Leu Tyr Ser Cys Asp Asp Cys Gly Arg Ser Phe
370 375 380
Arg Leu Glu Arg Phe Leu Arg Ala His Gln Arg His Asp Thr Gly Glu
385 390 395 400
Arg Pro Phe Thr Cys Ala Glu Cys Gly Lys Asn Phe Gly Lys Lys Thr
405 410 415
His Leu Val Ala His Ser Pro Val His Ser Gly Glu Arg Pro Phe Ala
420 425 430
Cys Glu Glu Cys Gly Arg Arg Phe Ser Gln Gly Ser His Leu Ala Ala
435 440 445
His Arg Pro Asp His Ala Pro Asp Arg Pro Phe Val Cys Pro Asp Cys
450 455 460
Gly Lys Ala Phe Arg His Lys Pro Tyr Leu Ala Arg His Arg Arg Ile
465 470 475 480
His Thr Gly Glu Lys Pro Tyr Val Cys Pro Asp Cys Gly Lys Ala Phe
485 490 495
Ser Gln Lys Ser Asn Leu Val Ser His Arg Arg Ile His Thr Gly Glu
500 505 510
Arg Pro Tyr Ala Cys Pro Asp Cys Asp Arg Ser Phe Ser Gln Lys Ser
515 520 525
Asn Leu Ile Thr His Arg Lys Ser His Ile Arg Asp Gly Ala Phe Cys
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cgc ttc cgg cac aag ccc aac ttg atc gct cac cgc cgc gtg cac acg
Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg Val His Thr
20 25 30

96

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35 40 45		
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Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly Glu Lys Pro		
50 55 60		
tac ccg tgc aaa gag tgc ggc cgc cgc ttc cgg cac aaa ccc aac ctg	240	
Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys Pro Asn Leu		
65 70 75 80		
ctg tct cac agc aag att cac aag cga tcc gag ggg tcg gcc cag gcc	288	
Leu Ser His Ser Lys Ile His Lys Arg Ser Glu Gly Ser Ala Gln Ala		
85 90 95		
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Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala Gly Pro Gln Glu Ser		
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35 40 45		
Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly Glu Lys Pro		
50 55 60		
Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys Pro Asn Leu		
65 70 75 80		
Leu Ser His Ser Lys Ile His Lys Arg Ser Glu Gly Ser Ala Gln Ala		
85 90 95		
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ctg cca gcc ggc ccc cag gag tcc gcg gcc gag ccc acc ccg gcg gta 96
Leu Pro Ala Gly Pro Gln Glu Ser Ala Ala Glu Pro Thr Pro Ala Val
20 25 30

cct ctg aaa ccg gcc cag gag ccg ccg cca ggg gcc ccg cca gag cac 144
Pro Leu Lys Pro Ala Gln Glu Pro Pro Pro Gly Ala Pro Pro Glu His
35 40 45

ccg cag gac ccg atc gaa gcc ccc ccc tcc ctc 177
Pro Gln Asp Pro Ile Glu Ala Pro Pro Ser Leu
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20 25 30
Pro Leu Lys Pro Ala Gln Glu Pro Pro Pro Gly Ala Pro Pro Glu His
35 40 45
Pro Gln Asp Pro Ile Glu Ala Pro Pro Ser Leu
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Trp Leu His Thr Arg Arg Cys Gln
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Ile Thr His Arg Lys Ser His Ile
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<223> Xaa is any amino acid.

<221> VARIANT
<222> (20)...(22)
<223> Xaa is any amino acid.

<221> VARIANT
<222> (24)...(24)
<223> Xaa is any amino acid.

<400> 47

Xaa Xaa Cys Xaa Xaa Cys Xaa Xaa Xaa Phe Xaa Xaa Xaa Xaa Xaa Leu
1 5 10 15
Xaa Xaa His Xaa Xaa Xaa His Xaa
20

<210> 48
<211> 702
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (1)...(702)

<400> 48

atg ctg gaa cgt cgt tgc agg ggc ccc ctg gcc atg ggc ctg gcc cag 48
Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Leu Ala Gln
1 5 10 15

ccc cga ctc ctt tct ggg ccc tcc cag gag tca ccc cag acc ctg ggg 96
Pro Arg Leu Leu Ser Gly Pro Ser Gln Glu Ser Pro Gln Thr Leu Gly
20 25 30

aag gag tcc cgc ggg ctg agg caa caa ggc acg tca gtg gcc cag tct 144
Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala Gln Ser
35 40 45

ggt gcc caa gcc cca ggc agg gcc cat cgc tgt gcc cac tgt cga agg 192
Gly Ala Gln Ala Pro Gly Arg Ala His Cys Ala His Cys Arg Arg

	50	55	60	
cac ttc cct ggc tgg gtg gct ctg tgg ctt cac acc cgc cgg tgc cag His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg Cys Gln				240
65	70		75	80
gcc cgg ctg ccc ttg ccc tgc cct gag tgt ggc cgt cgc ttt cgc cat Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe Arg His				288
85		90		95
gcc ccc ttc tta gca ctg cac cgc cag gtc cat gct gct gcc acc cca Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Thr Pro				336
100		105		110
gac ctg ggc ttt gcc tgc cac ctc tgt ggg cag agc ttc cga ggc tgg Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg Gly Trp				384
115		120		125
gtg gcc ctg gtt ctg cat ctg ctg gcc cat tca gct gca aag caa ccc Val Ala Leu Val Leu His Leu Leu Ala His Ser Ala Ala Lys Gln Pro				432
130		135		140
atc gct tgt ccc aaa tgc gag aga cgc ttc tgg cga cga aag cag ctt Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys Gln Leu				480
145		150		155
cga gct cat ctg cgg cgg tgc cac cct ccc gcc ccg gag gcc cgg ccc Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala Arg Pro				528
165		170		175
ttc ata tgc ggc aac tgt ggc cgg agc ttt gcc cag tgg gac cag cta Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp Gln Leu				576
180		185		190
gtt gcc cac aag cgg gtg cac gta gct gag gcc ctg gag gag gcc gca Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Ala Ala				624
195		200		205
gcc aag gct ctg ggg ccc cgg ccc agg ggc cgc ccc gcg gtg acc gcc Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val Thr Ala				672
210		215		220
ccc cgg ccc ggt gga gat gcc gtc gac cgc Pro Arg Pro Gly Gly Asp Ala Val Asp Arg				702
225		230		

<210> 49
<211> 234
<212> PRT
<213> Homo Sapiens

<400> 49
Met Leu Glu Arg Arg Cys Arg Gly Pro Leu Ala Met Gly Leu Ala Gln
1 5 10 15
Pro Arg Leu Leu Ser Gly Pro Ser Gln Glu Ser Pro Gln Thr Leu Gly
20 25 30
Lys Glu Ser Arg Gly Leu Arg Gln Gln Gly Thr Ser Val Ala Gln Ser
35 40 45

Gly Ala Gln Ala Pro Gly Arg Ala His Arg Cys Ala His Cys Arg Arg
50 55 60
His Phe Pro Gly Trp Val Ala Leu Trp Leu His Thr Arg Arg Cys Gln
65 70 75 80
Ala Arg Leu Pro Leu Pro Cys Pro Glu Cys Gly Arg Arg Phe Arg His
85 90 95
Ala Pro Phe Leu Ala Leu His Arg Gln Val His Ala Ala Ala Thr Pro
100 105 110
Asp Leu Gly Phe Ala Cys His Leu Cys Gly Gln Ser Phe Arg Gly Trp
115 120 125
Val Ala Leu Val Leu His Leu Leu Ala His Ser Ala Ala Lys Gln Pro
130 135 140
Ile Ala Cys Pro Lys Cys Glu Arg Arg Phe Trp Arg Arg Lys Gln Leu
145 150 155 160
Arg Ala His Leu Arg Arg Cys His Pro Pro Ala Pro Glu Ala Arg Pro
165 170 175
Phe Ile Cys Gly Asn Cys Gly Arg Ser Phe Ala Gln Trp Asp Gln Leu
180 185 190
Val Ala His Lys Arg Val His Val Ala Glu Ala Leu Glu Glu Ala Ala
195 200 205
Ala Lys Ala Leu Gly Pro Arg Pro Arg Gly Arg Pro Ala Val Thr Ala
210 215 220
Pro Arg Pro Gly Gly Asp Ala Val Asp Arg
225 230

<210> 50
<211> 441
<212> DNA
<213> Homo Sapiens

<220>
<221> CDS
<222> (1)...(441)

<400> 50

ggg gga gat gcc gtc gac cgc ccc ttc cag tgt gcc tgt tgt ggc aag 48
Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys Ala Cys Cys Gly Lys
1 5 10 15

cgc ttc cgg cac aag ccc aac ttg atc gct cac cgc cgc gtg cac acg 96
Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg Val His Thr
20 25 30

ggc gag cgg ccc cac cag tgc ccc gag tgc ggg aag cgc ttt acc aat 144
Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly Lys Arg Phe Thr Asn
35 40 45

aag ccc tat ctg act tcg cac cgg cgc atc cac acc ggc gag aag ccc 192
Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly Glu Lys Pro
50 55 60

tac ccg tgc aaa gag tgc ggc cgc cgc ttc cgg cac aaa ccc aac ctg 240
Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys Pro Asn Leu
65 70 75 80

ctg tct cac agc aag att cac aag cga tcc gag ggg tcg gcc cag gcc 288
Leu Ser His Ser Lys Ile His Lys Arg Ser Glu Gly Ser Ala Gln Ala
85 90 95

gcc ccc ggc ccg ggg agc ccc cag ctg cca gcc ggc ccc cag gag tcc	336
Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala Gly Pro Gln Glu Ser	
100 105 110	
gct gcc gag ccc acc ccg gct cct ctg aaa ccg gcc cag gag ccg	384
Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys Pro Ala Gln Glu Pro	
115 120 125	
ccg cca ggg gcc ccg cca gag cac ccg cag gac ccg atc gaa gcc ccc	432
Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp Pro Ile Glu Ala Pro	
130 135 140	
ccc tcc ctc	441
Pro Ser Leu	
145	

<210> 51
<211> 147
<212> PRT
<213> Homo Sapiens

<400> 51
Gly Gly Asp Ala Val Asp Arg Pro Phe Gln Cys Ala Cys Cys Gly Lys
1 5 10 15
Arg Phe Arg His Lys Pro Asn Leu Ile Ala His Arg Arg Val His Thr
20 25 30
Gly Glu Arg Pro His Gln Cys Pro Glu Cys Gly Lys Arg Phe Thr Asn
35 40 45
Lys Pro Tyr Leu Thr Ser His Arg Arg Ile His Thr Gly Glu Lys Pro
50 55 60
Tyr Pro Cys Lys Glu Cys Gly Arg Arg Phe Arg His Lys Pro Asn Leu
65 70 75 80
Leu Ser His Ser Lys Ile His Lys Arg Ser Glu Gly Ser Ala Gln Ala
85 90 95
Ala Pro Gly Pro Gly Ser Pro Gln Leu Pro Ala Gly Pro Gln Glu Ser
100 105 110
Ala Ala Glu Pro Thr Pro Ala Val Pro Leu Lys Pro Ala Gln Glu Pro
115 120 125
Pro Pro Gly Ala Pro Pro Glu His Pro Gln Asp Pro Ile Glu Ala Pro
130 135 140
Pro Ser Leu
145

<210> 52
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 52
aatttaccgt ttcttat 16

<210> 53
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 53
ccttccttct tattca 16

<210> 54
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 54
ttcatttgat tttatt 16

<210> 55
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 55
ttttataatt cctatt 16

<210> 56
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 56
tctaatttgc ttttta 16

<210> 57
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 57
tgtttgatt ttttat 16

<210> 58
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 58
tattttattt attaat

16

<210> 59
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 59
ttcttttttc ataaaat

16

<210> 60
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 60
tattatTTTA tgTTGA

16

<210> 61
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 61
tttttaaatt ttttta

16

<210> 62
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 62
gatgaatttt ttttta

16

<210> 63
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 63
tactttatgg ttaAGC

16

<210> 64

<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 64

ctattactgt tttcttg

16

<210> 65
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 65

tttttttagt ttctta

16

<210> 66
<211> 16
<212> DNA
<213> Artificial Sequence

<220>
<223> Synthetic

<400> 66

tactttatgg ttaacg

16

<210> 67
<211> 22
<212> DNA
<213> Cricetulus sp.

<400> 67
tttttttatt attattatta gt

22

<210> 68
<211> 72
<212> PRT
<213> Homo Sapiens

<400> 68
His Ser Lys Ile His Lys Arg Ser Glu Gly Ser Ala Gln Ala Ala Pro
1 5 10 15
Gly Pro Gly Ser Pro Gln Leu Pro Ala Gly Pro Gln Glu Ser Ala Ala
20 25 30
Glu Pro Thr Pro Ala Val Pro Leu Lys Pro Ala Gln Glu Pro Pro Pro
35 40 45
Gly Ala Pro Pro Glu His Pro Gln Asp Pro Ile Glu Ala Pro Pro Ser
50 55 60
Leu Tyr Ser Cys Asp Asp Cys Gly
65 70